SEQUENCE LISTING

(1) GENERAL INFORMATION:
    (i) APPLICANT: Arthur A. Branstrom
                        Donata R. Sizemore
                        Jerald C. Sadoff

    (ii) TITLE OF INVENTION: Bacterial Delivery System

    (iii) NUMBER OF SEQUENCES: 8

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: John Moran
        (B) STREET: USA MRMC - MCMR-JA
        (C) CITY: FORT DETRICK, FREDERICK
        (D) STATE: MARYLAND
        (E) COUNTRY: USA
        (F) ZIP: 21702-5012

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: Apple Macintosh
        (C) OPERATING SYSTEM: Macintosh 7.0
        (D) SOFTWARE: Microsoft Word

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Moran, John
        (B) REGISTRATION NUMBER: 26,313
        (C) REFERENCE/DOCKET NUMBER:

    (ix) TELECOMMUNICATION INFORMATION
        (A) TELEPHONE: (301) 619-2065
        (B) TELEFAX: (301) 619-7714

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1674 base pairs
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1

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     TCCATAATCA GGATCAATAA AACTGCTGCA GAAATGATTT        40

     CATTCATAAC TCAAATTCCC TGATAATTGC CGCGGACTTT        80

5    CTGCGTGCTA ACAAAGCAGG ATAAGTCGCA TTACTCATGG        120

     CTTCGCTATC ATTGATTAAT TTCACTTGCG ACTTTGGCTG        160

     CTTTTTGTAT GGTGAAAGAT GTGCCAAGAG GAGACCGGCA        200

     CATTTATACA GCACACATCT TTGCAGGAAA AAAACGCTTA        240

     TGAAAAATGT TGGTTTTATC GGCTGGCGCG GTATGGTCGG        280

10   CTCCGTTCTC ATGCAACGCA TGGTTGAAGA GCGCGACTTC        320

     GACGCCATTC GCCCTGTCTT CTTTTCTACT TCTCAGCTTG        360

     GCCAGGCTGC GCCGTCTTTT GGCGGAACCA CTGGCACACT        400

     TCAGGATGCC TTTGATCTGG AGGCGCTAAA GGCCCTCGAT        440

     ATCATTGTGA CCTGTCAGGG CGGCGATTAT ACCAACGAAA        480

15   TCTATCCAAA GCTTCGTGAA AGCGGATGGC AAGGTTACTG        520

     GATTGACGCA GCATCGTCTC TGCGCATGAA AGATGACGCC        560

     ATCATCATTC TTGACCCCGT CAATCAGGAC GTCATTACCG        600

     ACGGATTAAA TAATGGCATC AGGACTTTTG TTGGCGGTAA        640

     CTGTACCGTA AGCCTGATGT TGATGTCGTT GGGTGGTTTA        680

20   TTCGCCAATG ATCTTGTTGA TTGGGTGTCC GTTGCAACCT        720

     ACCAGGCCGC TTCCGGCGGT GGTGCGCGAC ATATGCGTGA        760

     GTTATTAACC CAGATGGGCC ATCTGTATGG CCATGTGGCA        800

     GATGAACTCG CGACCCCGTC CTCTGCTATT CTCGATATCG        840

     AACGCAAAGT CACAACCTTA ACCCGTAGCG GTGAGCTGCC        880

25   GGTGGATAAC TTTGGCGTGC CGCTGGCGGG TAGCCTGATT        920

     CCGTGGATCG ACAAACAGCT CGATAACGGT CAGAGCCGCG        960

     AAGAGTGGAA AGGGCAGGCG GAAACCAACA AGATCCTCAA        1000
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CACATCTTCC GTAATTCCGG TAGATGGTTT ATGTGTGCGT   1040

GTCGGGGCAT TGCGCTGCCA CAGCCAGGCA TTCACTATTA   1080

AATTGAAAAA AGATGTGTCT ATTCCGACCG TGGAAGAACT   1120

GCTGGCTGCG CACAATCCGT GGGCGAAAGT CGTTCCGAAC   1160

GATCGGGAAA TCACTATGCG TGAGCTAACC CCAGCTGCCG   1200

TTACCGGCAC GCTGACCACG CCGGTAGGCC GCCTGCGTAA   1240

GCTGAATATG GGACCAGAGT TCCTGTCAGC CTTTACCGTG   1280

GGCGACCAGC TGCTGTGGGG GGCCGCGGAG CCGCTGCGTC   1320

GGATGCTTCG TCAACTGGCG TAATCTTTAT TCATTAAATC   1360

TGGGGCGCGA TGCCGCCCCT GTTAGTGCGT AATACAGGAG   1400

TAAGCGCAGA TGTTTCATGA TTTACCGGGA GTTAAATAGA   1440

GCATTGGCTA TTCTTTAAGG GTGGCTGAAT ACATGAGTAT   1480

TCACAGCCTT ACCTGAAGTG AGGACGACGC AGAGAGGATG   1520

CACAGAGTGC TGCGCCGTTC AGGTCAAAAA AATGTCACAA   1560

CCAGAAGTCA AAAATCCAAT TGGATGGGGT GACACAATAA   1600

AACAGGAAGA CAAGCATGTC CGATCGTATC GATAGAGACG   1640

TGATTAACGC GCTAATTGCA GGCCATTTTG CGGA   1674

(3) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1121 base pairs
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear
    (ii) MOLECULE TYPE: Other nucleic acid
        (A) DESCRIPTION: The *E. coli asd* gene coding for β-aspartic semialdehyde dehydrogenase identified in SEQ ID NO:1 was modified by deleting 553 bp from position 439 to 991.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

TCCATAATCA GGATCAATAA AACTGCTGCA GAAATGATTT   40

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        CATTCATAAC TCAAATTCCC TGATAATTGC CGCGGACTTT      80
        CTGCGTGCTA ACAAAGCAGG ATAAGTCGCA TTACTCATGG      120
        CTTCGCTATC ATTGATTAAT TTCACTTGCG ACTTTGGCTG      160
        CTTTTTGTAT GGTGAAAGAT GTGCCAAGAG GAGACCGGCA      200
5       CATTTATACA GCACACATCT TTGCAGGAAA AAAACGCTTA      240
        TGAAAAATGT TGGTTTTATC GGCTGGCGCG GTATGGTCGG      280
        CTCCGTTCTC ATGCAACGCA TGGTTGAAGA GCGCGACTTC      320
        GACGCCATTC GCCCTGTCTT CTTTTCTACT TCTCAGCTTG      360
        GCCAGGCTGC GCCGTCTTTT GGCGGAACCA CTGGCACACT      400
10      TCAGGATGCC TTTGATCTGG AGGCGCTAAA GGCCCTCGGA      440
        TCCTCAACAC ATCTTCCGTA ATTCCGGTAG ATGGTTTATG      480
        TGTGCGTGTC GGGGCATTGC GCTGCCACAG CCAGGCATTC      520
        ACTATTAAAT TGAAAAAGA TGTGTCTATT CCGACCGTGG       560
        AAGAACTGCT GGCTGCGCAC AATCCGTGGG CGAAAGTCGT      600
15      TCCGAACGAT CGGGAAATCA CTATGCGTGA GCTAACCCCA      640
        GCTGCCGTTA CCGGCACGCT GACCACGCCG GTAGGCCGCC      680
        TGCGTAAGCT GAATATGGGA CCAGAGTTCC TGTCAGCCTT      720
        TACCGTGGGC GACCAGCTGC TGTGGGGGGC CGCGGAGCCG      760
        CTGCGTCGGA TGCTTCGTCA ACTGGCGTAA TCTTTATTCA      800
20      TTAAATCTGG GCGCGATGC CGCCCCTGTT AGTGCGTAAT       840
        ACAGGAGTAA GCGCAGATGT TTCATGATTT ACCGGGAGTT      880
        AAATAGAGCA TTGGCTATTC TTTAAGGGTG GCTGAATACA      920
        TGAGTATTCA CAGCCTTACC TGAAGTGAGG ACGACGCAGA      960
        GAGGATGCAC AGAGTGCTGC GCCGTTCAGG TCAAAAAAAT      1000
25      GTCACAACCA GAAGTCAAAA ATCCAATTGG ATGGGGTGAC      1040
        ACAATAAAAC AGGAAGACAA GCATGTCCGA TCGTATCGAT      1080
        AGAGACGTGA TTAACGCGCT AATTGCAGGC CATTTTGCGG      1120
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(4) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

AGATCTCCCT GATAATTGCC GC   22

(5) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 base pairs
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

AGATCTCGCT TACTCCTGTA TTACGC   26

(6) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

CGAGGGCCTT TAGCGCCTCC   20

(7) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

GATCCTCAAC ACATCTTCCG

5   (8) INFORMATION FOR SEQ ID NO:7:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 base pairs
            (B) TYPE: Nucleic acid
10   (C) STRANDEDNESS: Double
            (D) TOPOLOGY: Linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

15   GAGCTCCCCT GATAATTGCC GC   22

    (9) INFORMATION FOR SEQ ID NO:8:

20   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 26 base pairs
            (B) TYPE: Nucleic acid
            (C) STRANDEDNESS: Double
25   (D) TOPOLOGY: Linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8
                                                              26
30   GTCGACCGCT TACTCCTGTA TTACGC

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